

GTCAATATGCTGTTCAGTCAATGGCAACTGGCAGCAGCCTCGGGCTCTGTCTGGAGTCTCTGGCATCCATTTGGACACCGGCAGGCAC	90
M L F K S W Q L A A A S G L L S G V L G I P M D T G S H	28
CCATTGAGGCTGTGTGATCCCGAAGTGAAGACTGAGGTCTTGGCTGACTCCCTCTCTGCTGCAGCAGGCGATGACGACTGGGAGTCACT	180
P I E A V D P E V K T E V F A D S L L A A A G D D D W E S P	58
CCATACAACCTTGCTTTACAGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGATGATCATTTACCAACCTCTGTCAACCGGCAAGGAC	270
P Y N L L Y R N A L P I P P V K Q P K M I I T N P V T G K D	88
ATTTGGTACTATGAGATCGAGATCAAGCCATTTTCAGCAAAGGATTTACCCCACTTTGGGCGCTGCCACTCTCTGTGGCTACGATGGCATG	360
I W Y Y E I E I K P F Q Q R I Y P T L R P A T L V G Y D G M	118
AGCCCTGGTCTACTTTCAATGTTCACAGAGGAACAGAGACTGTAGTTAGGTTTCATCAACAATGCCACCGTGGAGAACTGGTTCATCTG	450
S P G P T F N V P R G T E T V V R F I N N A T V E N S V H L	148
CAGGCTCCCATCGCGTGGCGCTTTTCGATGGTTGGGCTGAAGATGTGAACCTTCCTGGCGAGTACAAGGATTACTACTTTTCCCAACTAC	540
H G S P S R A P F D G W A E D V T F P G E Y K D Y Y F P N Y	178
CAATCCGCGCGCTTCTGTGGTACCATGACCAAGCTTTTCATGAAGACTGCTGAGAATGCCACTTTTGGTTCAGGCTGGCGCTACATTATC	630
Q S A R L L W Y H D H A F M K T A E N A Y F G Q A G A Y I I	208
AACGACGAGGCTGAGGATGCTCTGGTCTTTCCTAGTGGCTATGGCGAGTTGGATATCCCTCTGATCTGACGGCCAAGTACTATAAGCC	720
N D E A E D A L G L P S G Y G E F D I P L I L T A K Y Y N A	238
GATGGTACCTTCGCTTCGACCGAGGGTGAGGACCAGCACTGTGGGAGATGTCAATCATGTCAACGGACAGCCATGGCTTTTCTTTAAC	810
D G T L R S T E G E D Q D L W G D V I H V N G Q P W P F L N	268
GTCCAGCCCGCAAGTACCGTTTCCGATTCTCTCAACGCTGCCGTGTCTCTGTCTTGGCTCTCTACCTGCTCAGGACCAGCTCTCCCAAC	900
V Q P R K Y R F R F L N A A V S R A W L L Y L V R T S S P N	298
GTCAGAACTCTTTTCAAGTCAATGCCCTCTGATGCTGGTCTCTCTCAAGCCCCCGTTCAGACCTCTAACTCTACCTTCTGTGTGGCGAG	990
V R I P F Q V I A S D A G L L Q A P V Q T S N L Y L A V A E	328
CGTTACGAGATCATTATTGACTTTCACCAACTTTTGGTGGCCAGACTCTTTGACCTGGCGAACGTTTCTGAGACCAACGATGTCCGGACGAG	1080
R Y E I I I D F T N F A G Q T L D L R N V A E T N D V G D E	358
GATGAGTACGCTCGCACTCTCGAGGTGATGCCCTTCTGTCTGCTCAGCTCTGGCACTGTGTGAGGACAACAGCCAGGTCCCTCCACTCTCCGT	1170
D E Y A R T L E V M R F V V S S G T V E D N S Q V P S T L R	388
GACGTTCTTTTCCCTCTCTCACAAGGAAGGCCCGCCGACAAGCACTTCAAGTTTGAACCGCAGCAACGGACACTACCTGATCAACGATGTT	1260
D V P F P P P H K E G P A D K H F K F E R S N G H Y L I N D V	418
GGCTTTGGCGATGTCAATGAGCGTGTCTCTGGCCAAGCCCGAGCTGGGCAACGTTGAGGTCTGGGAGCTCGAGAACTCTCTGGAGGCTGG	1350
G F A D V N E R V L A K P E L G T V E V W E L E N S S G G W	448
AGCCACCCCGTCCACATTCACCTTGTGTGACTTTCAGATCTCTCAAGCGAACTGGTGGTGTGGCCAGGTCATGCCCTACGAGTCTGCTGGT	1440
S H P V H I H L V D F K I L K R T G G R G Q V M P Y E S A G	478
CTTAAGGATGTGTCTGTGTGGGCGAGGGGTGAGACCTTGACCATGAGGCGCACTACCAACCTGGACTGGAGCTTACATGTGGCACTGT	1530
L K D V V W L G R G E T L T I E A H Y Q P W T G A Y M W H C	508
CACAACCTCATTCACGAGGATAACGACATGATGGCTGTATTCAACGTCAACGCCATGGAGGAGAAGGGATATCTTCAGGAGGACTTCGAG	1620
H N L I H E D N D M M A V F N V T A M E E K G Y L Q E D F E	538
GACCCCATGAACCCCAAGTGGCGCGCGCTTCTTACAACCGCAACGACTTCATGCTCGCGCTGGAACTTCTCCGCGGAGTCCATCACT	1710
D P M N P K W R A V P Y N R N D F H A R A G N F S A E S I T	568
GCCCGAGTGCAGGAGCTGGCGGAGGAGCGGTACAACCGCCTCGATGAGATCTTGGAGGATCTTGAATCGAGGAGTAA	1791
A R V Q E L A E Q E P Y N R L D E I L E D L G I E E	594

Figure 1

CTGGCTAGCC	TCACTTGGTA	GACAGCCCTG	ACAGCCCTAC	TGGCTGGGGG	TOGAAAGGCC	AGTCAATATC	TTGGTCACTG	80
CTAATAGTTC	CTTGCTAGCC	GCAAAAAGCT	CCTTGCCGAA	GGGGCACAGA	CTATCAAGTG	AGACATATAG	GATGCATGTC	160
TTTCATAGCC	ACAGTTAGGG	TGGTGACCTA	CTCGAAGAGG	CCCGACTTGG	CATGCATAGC	ACATGTGCGT	TCCATGCAAC	240
ATGTATGCGC	ACATCGGCGA	TCAGGCACCC	TCTGATGCA	GAATAGAACC	CCCGTGGTTT	CCTTTTGTFTT	CTTTTCCTTT	320
CTCAACGACG	CGTGAGCGTG	GTTAACTTGA	GCAAGGCCGA	GTGGTCTGT	CACGAGGTTA	CCATCGAACT	CTCTTCTTTC	400
CCAATCATGA	CCTGCCCCCC	GAGTTTAGCC	CCCATCAACG	CTGTGAAATC	CACCTTGATA	ATCCTAGCCT	AGTGCTACTC	480
TTCAATAGTT	GCTCCTGATG	GGGCACTTTG	GTACACATTG	CCTGGTFTYCT	CCTACCTCGT	TCTCTTCCGC	ATCAAGCCTC	560
TATGCCCCGAC	GACAACACCT	CATTGGCCCC	GACCACTTTG	AGCGCGCAG	CACCTTCCGC	CCGAAGGAGT	TGATAACACC	640
CTTCACCCCT	GCCCCAATGAT	GGAGTTTGTG	TCTATTTTGT	ATGATCACCT	CACATTCACT	AGATCACCGA	TCCTGGAAGA	720
GGGTGTGGAA	GCCAGAACAG	CTTGTCCCTG	TTCTTGCAGA	CTCAGGTCAG	CTCCTAGCGG	CTATCACAGC	TCAGGATTAT	800
CAAGTCCCGT	AAAGTCCAGA	CCCTTTTTCAT	TGTATGATGC	TGCCATAATT	GCGCTATCTC	TATGCGGTAG	CAGCCGTCTT	880
GGCTACAACCT	GGCTGCCATG	GCTGAAGCAT	CGTGAGATCT	ATAAAGGTCT	CCGAATCCCT	GGTGAAGTCA	GAATCGTCTC	960
TCCACACCAG	TCAACAACAA	GCTTCTTTTCT	CTTACAGCTT	AGCCTGAGCA	CATTTCACAGA	ACTCTTCCCT	TCTTTTTCGT	1040
AATATGCTGT	TCAAGTCAATG	GCAACTGGCA	GCAGCCCTCG	GGCTCCTGTG	TGGAGTCCCT	GGCATCCCGA	TGGACACCGG	1120
CAGCCACCCC	ATTGAGGCTG	TTGATCCCGA	AGTGAAGACT	GAGGTCTTGG	CTGACTCCCT	CCTTGCTGCA	GCAGGCGATG	1200
ACGACTGGGA	GTACACCTCA	TACAACCTTG	TTTACAGGTG	AGACACCTGT	CCCACCTGTT	TTCCCTCGAT	AACTAACTCT	1280
TATAGGAATG	CCCTGCCAAT	TCCACCTGTC	AAGCAGCCCA	AGATGTATGT	CTTTGATTTT	CTACGAAGCA	ACTCGGCCCC	1360
GACTAATGTA	TTCTAGGATC	ATTACCAACC	CTGTCAACGG	CAAGGACATT	TGGTACTATG	AGATCGAGAT	CAAGCCATT	1440
CAGCAAAGGG	TGAGTTTGTCT	CAGAAACCTT	GTGGTAAATTA	ATCATTTGTTA	CTGACCCCTT	CAGATTTACC	CCACCTTGCG	1520
CCCTGCCACT	CTCGTCGGCT	ACGATGGCAT	GAGCCCTGGT	CCTACTTTCA	ATGTTCCCGA	AGGAACAGAG	ACTGTAGTTA	1600
GGTTTCATCAA	CAATTGCCAC	GTGGAGAATC	CGGTCCATCT	GCACGGCTCC	CCATCGCGTG	CCCTTTTCGA	TGGTTGGGCT	1680
GAAGATGTGA	CCTTCCCTGG	CGAGTACAG	GATTACTACT	TTCCCAACTA	CCAATCCGCC	CGCCTTCTGT	GGTACCATGA	1760
CCACGCTTTC	ATGAAGGTAT	GCTACGAGCC	TTTATCTTTC	TTGGCTTAAC	TTGGCTTAAC	AACTTCTTTC	CGTAGACTGC	1840
TGAGAATGCC	TACTTTTGGT	AGGCTGGGCG	CTACATTTATC	AACGACGAGG	CTGAGGATGC	TCTCGGTCTT	CCTAGTGGCT	1920
ATGGCGAGTT	CGATATCCCT	CTGATCCTGA	CGGCCAAGTA	CTATAACGCC	GATGGTACCC	TGCGTTTCGAC	CGAGGGTGAG	2000
GACCAGGACC	TGTGGGGAGA	TGTATCCAT	GTCAACGGAC	AGCCATGGCC	TTTCTTTAAC	GTCCAGCCCC	GCAAGTACCG	2080
TTTCCGATT	CTCAACGCTG	CCGTGTCTCG	TGCTTGGCTC	CTCTACCTCG	TCAGGACCAG	CTCTCCCAAC	GTGAGAATTC	2160
CTTTCCAAGT	CATTGCCCTCT	GATGCTGGTC	TCCTTCAAGC	CCCGTTTCAG	ACCTCTAAC	TCTACCTTGC	TGTTGCCGAG	2240
CGTTACGAGA	TCATTATTGG	TATGCCCTCC	CCTCTCACGA	ATGAGTCAAG	AACTCTAAGA	CTAACACTTG	TAGACTTCAC	2320
CAACTTTGCT	GGCCAGACTC	TTGACCTGCG	CAACGTTGCT	GAGACCAACG	ATGTCCGGCGA	CGAGGATGAG	TACGCTCGCA	2400
CTCTCGAGGT	GATGCGCTTC	GTGCTCAGCT	CTGGCCTGT	TGAGGACAAC	AGCCAGGTCC	CCTCCACTCT	CCGTGACGTT	2480
CCTTTCCCTC	CTCACAAGGA	AGGCCCCGCC	GACAAGCACT	TCAAGTTTGA	ACGCAGCAAC	GGACACTACC	TGATCAACGA	2560
TGTTTGGCTTT	GCCGATGTCA	ATGAGCGTGT	CCTGGCCAAG	CCCGAGCTCG	GCACCGTTGA	GGTCTGGGAG	CTCGAGAAT	2640
CCTCTGGAGG	CTGGAGCCAC	CCCGTCCACA	TTACACCTGT	TGACTTTAAG	ATCCTCAAGC	GAAGTGGTGG	TCGTGGCCAG	2720
GTCAATGCCCT	ACGAGTCTGC	TGGTCTTTAAG	GATGTCTGCT	GGTTGGGCAG	GGGTGAGACC	CTGACCATCG	AGGCCCACTA	2800
CCAACCCCTG	ACTGGAGCTT	ACATGTGGCA	CTGTACAAC	CTCATTCAGC	AGGATAACGA	CATGATGGCT	GTATTCAACG	2880
TCACCCCAT	GGAGGAGAAG	GGATATCTTC	AGGAGGACTT	CGAGGACCCC	ATGAACCCCA	AGTGGCGCGC	CGTTCCCTTAC	2960
AACCGCAACG	ACTTCCATGC	TCCGCGCTGA	AACCTTCTCC	CCGAGTCCAT	CATGCCCCGA	GTGCAGGAGC	TGGCCGAGCA	3040
GGAGCGGTAC	AACCGCCTCG	ATGAGATCCT	GGAGGATCTT	GGAATCGAGG	AGTAAACCCC	GAGCCACAAG	CTCTACAATC	3120
GTTTTGAGTC	TTAAGACGAG	GCTCTTGGTG	CGTATTTCTT	TCTTCCCTAC	GGGGAACTCC	GCTGTCCACT	GCGATGTGAA	3200
GGACCATCAC	AAAGCAACGT	ATATATTGGA	CTCACCCTG	TCATTACCGC	CCACTTGTAC	CTATTGCAAT	CTTGTTCAAA	3280
CTTTTCTAGT	GCGAGAGTGT	CCATAGTCAA	GAAACGCCCA	TAGGGCTATC	GTCTAAACTG	AACTATTGTG	TGGTCTGTGA	3360
CGTGGAGTAG	ATGTCAATTG	TGATGAGACA	CAGTAAATAC	GGTATATCTT	TTCTTAGGAC	TACAGGATCA	GTTTCTCATG	3440
AGATTACATC	CGTCTAATGT	TTGTCCATGA	GAGTCTAGCT	AAGGTTGAGA	ATGCATCAGA	CGGAATCAT	TGATGCTCTC	3520
AGCTCGTATT	ACCGATGTAA	GACAAGTTAG	GTAAGTTGCT	TGGTATCCGA	AAATGACTCA	GGCTCCCTCA	TTAGGTTTGA	3600
TGTGAAAACC	TTACAGCACT	CATGGGTGTT	GGGACCAAA	CATCCATACC	TGATTTTGTAT	AACTGACCTG	GGTCAAT	3677

Figure 2

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1 .....MFKHTLGAAALSLLFNSNAVQA.SVPETSPATGHLFKRV 39
      |         |         |         |         |
1 MLFKSWQLAAASGLLSGVLGIPMDTGSHPIEAVDPEVKTEVFADSLAAA 50

40 AQISPOYFMFTV....PLPIPPVKQPRLTIVINPANGQETWYYEVEIKPFT 85
      |         |||||         |||| | |||| |||||
51 GDDWESPPYNLLYRNALPIPPVKQPKMITINPVTGKDIWYYEIEIKPFQ 100

86 HQVYPDLGSADLVGYDGMSPGPTFQVPRGVEIVVRFINNAEAPNSVHLHG 135
      || | | ||||| ||||| ||||| ||||| |||||
101 QRLYPTLRPATLVGYDGMSPGPTFNVPRGIEIVVRFINNATVENSVHLHG 150

136 SFSRAAFDGAEDITEPGSFKDYYPNRQSARTLWYHDHAMHTTAENAYR 185
      | ||| ||||| | || |||| | |||| ||||| |||||
151 SPSRAPFDGAEDVTFRGEYKDYFPPNYQSARLLWYHDHAFMKTAEAYF 200

186 GQAGLYMLTDPADALNLP SGYGEFDIPMILTSKQYTANGNLVTINGELN 235
      |||| | | |||| | ||||| |||| | || | || |
201 GQAGAYIINDEAEDALGLPSGYGEFDIPLILITAKYYNADGTLRSTEGEDQ 250

236 SFWGDVIHVNGQPWPFFKNVEPRKYRFRFLDAAVSRSGLYFADIDAIDTR 285
      ||||| ||||| || ||||| ||||| |||| | |
251 DLWGDVIHVNGQPWPFILNVQPRKYRFRFLNAAVSRALLYLVRTSSPNVR 300

286 LPFKVIASDSGLLEHPADTSLLYISMAERYEVVDFSDYAGKTIELRLNG 335
      || ||||| || | || || |||| | || || | ||
301 IPFQVIASDAGLLQAPVQTSNLYLAVAERYEIIIDFINFAGQILDLRNV. 349

336 GSIGGIGTDTIDYDNDKVMRFWADDITQPDTSVVPANLRDVFPSPPTIN 385
      | | | ||||| | | |||| | |||||
350 AETNDVGDEDEYARTILEVMRFVSSGIVE.DNSQVPSTLRDVFPFPHKEG 398

386 .TPRQFRFRGTGPTWTINGVAFADVQNRLLANVPVGIVERWELINAGNGW 434
      | | | || |||| | || |||| | || |
399 PADKHFKFERSNGHYLINDVGFADVNERVLAKPELGTVEWELENSSGGW 448

435 THPIHIHLVDFKVISRTSGNNARTVMPIYES.GLKDVVWLGRRETWVEAH 483
      || ||||| || | |||| | ||||| ||||| || ||
449 SHPVHIHLVDFKILKRTGGRG..QVMPYESAGLKDVVWLGRGETITTEAH 496

484 YAPFPGVYMFHCHNLIHEDHDMMAAFNATVLPDYGYNATVFVDPMEELWQ 533
      | | | ||||| |||| | || | || | || |
497 YQPWTGAYMWHCHNLIHEDNDMAVFNVTAMEEKGYLQEDFEDFNNPKWR 546

534 ARPYELGEFQAQSGQFSVQAVIERIQTMAEYRYPYAADE..... 572
      || | | || | || | || | || |
547 AVPYNRNDFHARAGNFSAESITARVQELAEQEPYNRLDEILEDLGTEE 594

```

Figure 3: protein sequences alignment of Bilirubin oxidase (top sequence) with Stachybotrys oxidase (bottom sequence).

Figure 3

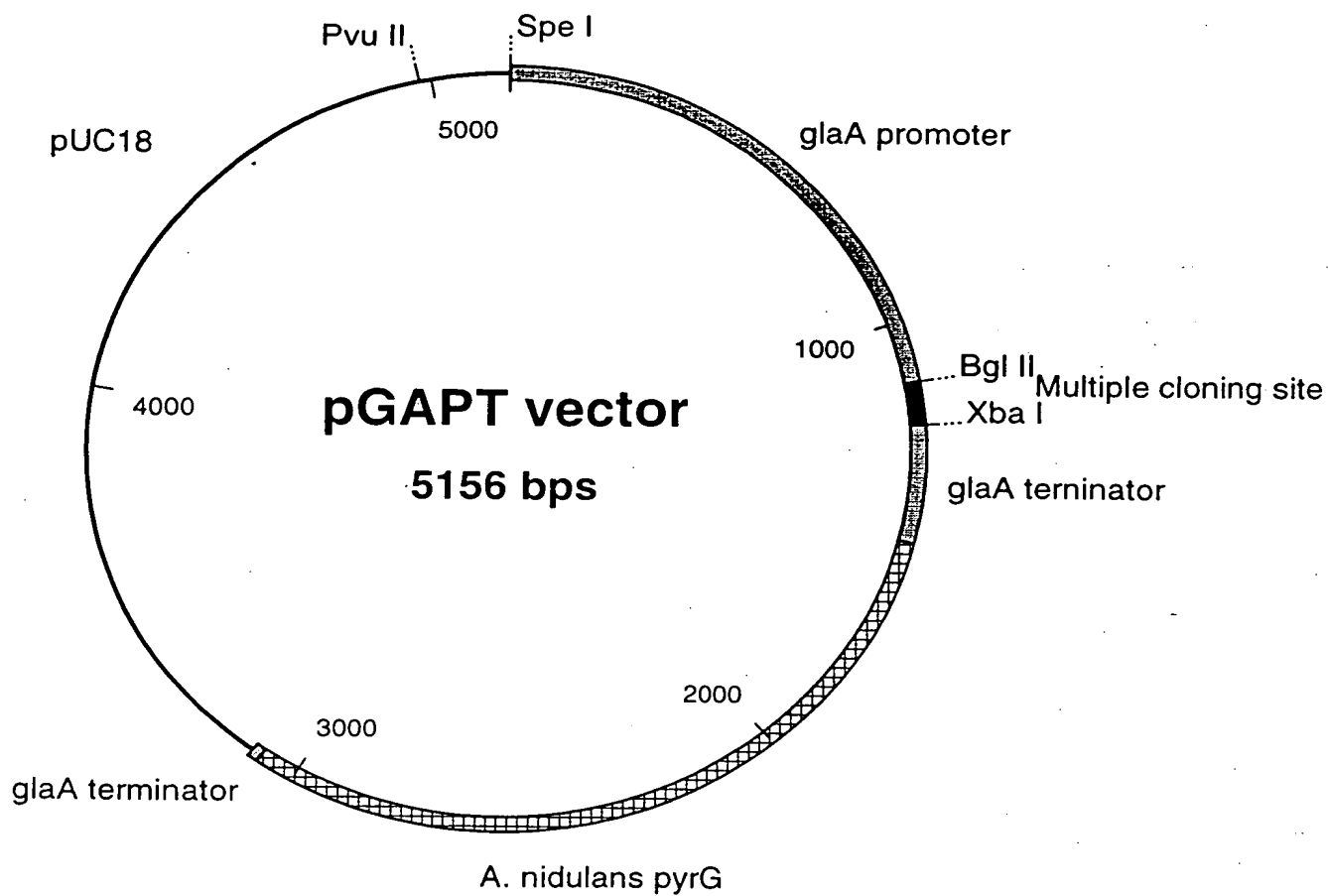


Figure 4

AGATCTAATA TGCTGTTCAA GTCATGGCAA CTGGCAGCAG CCTCCGGGCT CCTGTCTGGA 60
 GTCCTCGGCA TCCCGATGGA CACCGGCAGC CACCCCATTTG AGGCTGTTGA TCCCGAAGTG 120
 AAGACTGAGG TCTTCGCTGA CTCCCTCCTT GCTGCAGCAG GCGATGACGA CTGGGAGTCA 180
 CCTCCATACA ACTTGCTTTA CAGGTGAGAC ACCTGTCCCA CCTGTTTTTC CTGATAACT 240
 AACTCTTATA GGAATGCCCT GCCAATTCCA CCTGTCAAGC AGCCCAAGAT GTATGTCCTT 300
 GATTTTCTAC GAAGCAACTC GGCCCCGACT AATGTATTCT AGGATCATT AACAACCTGT 360
 CACCGGCAAG GACATTTGGT ACTATGAGAT CGAGATCAAG CCATTTTCAGC AAAGGGTGAG 420
 TTTGCTCAGA AACCTTGTTG TAATTAATCA TTGTTACTGA CCCTTTTCAGA TTTACCCAC 480
 CTTGCGCCCT GCCACTCTCG TCGGCTACGA TGGCATGAGC CCTGGTCTTA CTTTCAATGT 540
 TCCCAGAGGA ACAGAGACTG TAGTTAGGTT CATCAACAAT GCCACCGTGG AGAACTCGGT 600
 CCATCTGCAC GGCTCCCAT CGCGTGGCCC TTTCGATGGT TGGGCTGAAG ATGTGACCTT 660
 CCCTGGCGAG TACAAGGATT ACTACTTTTC CAACTACCAA TCCGCCCGCC TTCTGTGGTA 720
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 CTAACCAACT TCCTTTCTGA GACTGCTGAG AATGCCTACT TTGGTCAGGC TGGCGCCTAC 840
 ATTATCAACG ACGAGGCTGA GGATGCTCTC GGTCCTCTTA GTGGCTATGG CGAGTTCTGAT 900
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 CACAACCTCA TTCACGAGGA TAACGACATG ATGGCTGTAT TCAACGTCAC CGCCATGGAG 1860
 GAGAAGGGAT ATCTTCAGGA GGAATTGAG GACCCCATGA ACCCAAGTG GCGCGCCGT 1920
 CCTTACAACC GCAACGACTT CCATGCTCGC GCTGGAACT TCTCCGCCGA GTCCATCACT 1980
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 GATCTTGGA TCGAGGAGTA GTCTAGA 2067

Figure 5

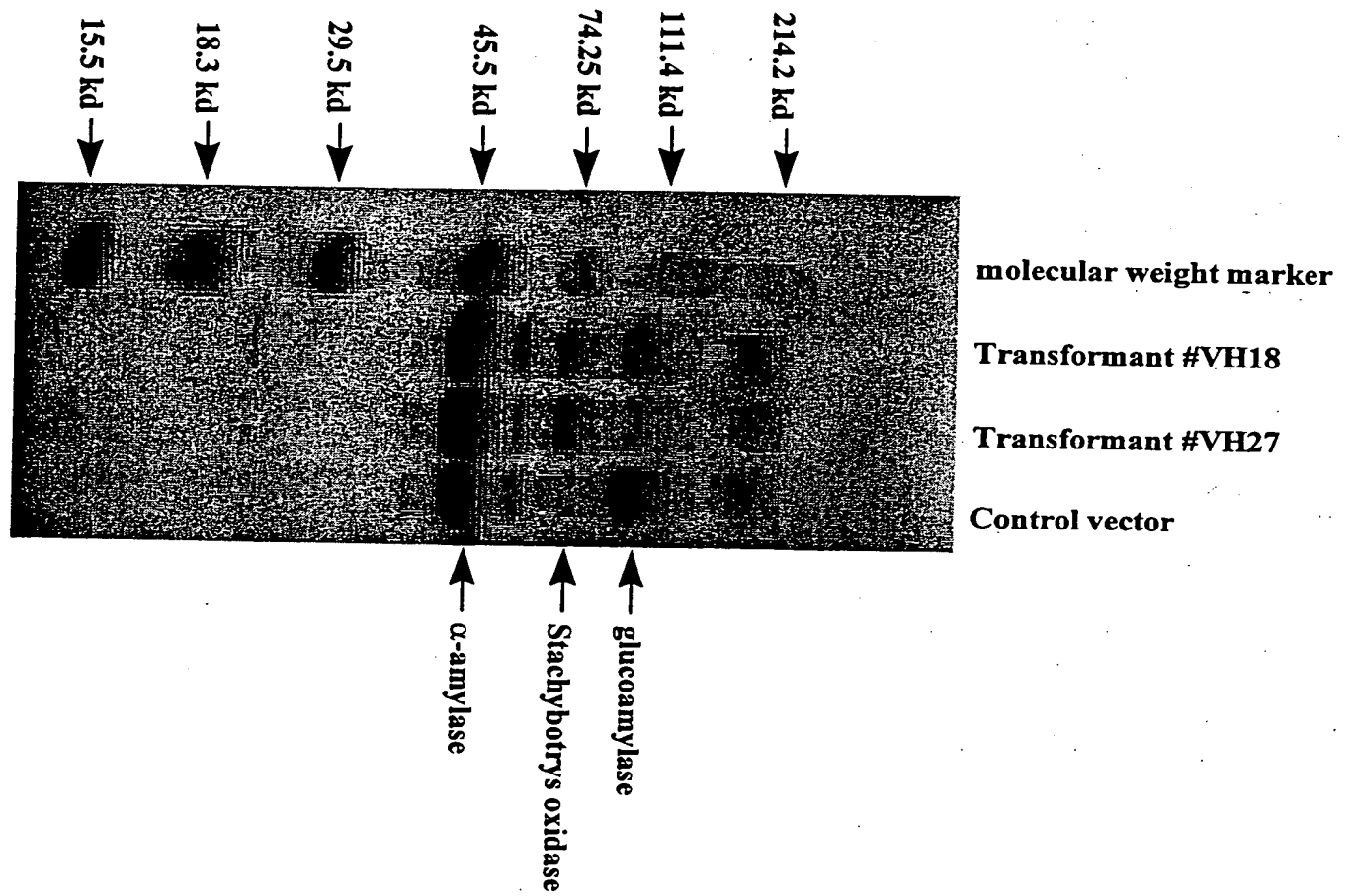


Figure 6